

**AMENDMENTS TO THE CLAIMS:**

This listing of claims will replace all prior versions and listings of claims in the application:

Claims 1-4 (Canceled).

5. (Presently Amended) ~~An~~ The isolated nucleic acid ~~molecule comprising the polynucleotide sequence~~ according to claim 18 selected from SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, and SEQ ID NO: 22.

6. (Presently Amended) A method of detecting prostate cancer ~~in a patient~~, the method comprising:

- (a) detecting hybridization between a nucleic acid comprising at least 10 contiguous nucleotides of SEQ ID NO:1 and a PCGEM1 mRNA nucleic acid in a biological sample ~~from the patient~~; and
- (b) correlating the amount of the PCGEM1 mRNA nucleic acid in the biological sample with the presence of prostate cancer ~~in the patient~~.

7. (Presently Amended) The method according to claim 6, ~~wherein step (a)~~  
~~includes further comprising before detecting hybridization:~~

- (a) isolating RNA from the biological sample; and
- (b) amplifying a the PCGEM1 ~~cDNA molecule~~ nucleic acid;
- ~~(c) incubating the PCGEM1 cDNA with the nucleic acid according to~~  
~~claim 1 or 5; and~~
- ~~(d) detecting hybridization between the PCGEM1 cDNA and the~~  
~~nucleic acid.~~

8. (Presently Amended) The method according to claim 7, wherein the  
PCGEM1 ~~cDNA~~ nucleic acid is amplified with at least two nucleotide sequences  
selected from SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID  
NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO:  
15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20,  
SEQ ID NO: 21, and SEQ ID NO: 22.

9. (Original) The method according to claim 8, wherein the at least two  
nucleotide sequences are SEQ ID NO:15 and SEQ ID NO:22.

10. (Original) A method according to claim 6, wherein the biological sample is  
selected from blood, urine, and prostate tissue.

11. (Original) The method according to claim 10, wherein the biological sample  
is blood.

Claims 12-17 (Canceled).

18. (New) An isolated nucleic acid, wherein the nucleic acid comprises at least about 17 contiguous nucleotides of SEQ ID NO:1.

19. (New) The isolated nucleic acid according to claim 18, wherein the nucleic acid comprises at least 20 nucleic acids.

20. (New) The isolated nucleic acid according to claim 19, wherein the nucleic acid comprises at least 30 nucleic acids.

21. (New) The isolated nucleic acid according to claim 18, wherein the nucleic acid comprises at least 60 nucleic acids.

22. (New) A method of detecting a PCGEM1 nucleic acid in a biological sample, comprising:

combining the biological sample with a nucleic acid comprising at least 10 contiguous nucleotides of SEQ ID NO:1 under hybridizing conditions; and

detecting hybridization between the nucleic acid comprising at least 10 contiguous nucleotides of SEQ ID NO:1 and the PCGEM1 nucleic acid in the biological sample, wherein hybridization indicates the presence of the PCGEM1 nucleic acid in the biological sample.

23. (New) The method of claim 22, further comprising a step of amplifying the PCGEM1 nucleic acid before combining the biological sample with the nucleic acid comprising at least 10 contiguous nucleotides of SEQ ID NO:1.

24. (New) A method according to claim 22, wherein the biological sample is selected from blood, urine, and prostate tissue.

25. (New) The method of claim 22, wherein the biological sample is prostate tissue.

26. (New) The method of claim 22, wherein the biological sample is blood.

27. (New) The method of claim 22, wherein the nucleic acid comprises at least about 17 contiguous nucleotides of SEQ ID NO:1.

28. (New) The method according to claim 22, wherein the nucleic acid comprises at least 20 nucleic acids of SEQ ID NO:1.

29. (New) The method according to claim 22, wherein the nucleic acid comprises at least 30 nucleic acids of SEQ ID NO:1.

30. (New) The method according to claim 22, wherein the nucleic acid comprises at least 60 nucleic acids of SEQ ID NO:1.

31. (New) The method of claim 6, wherein the nucleic acid comprises at least about 17 contiguous nucleotides of SEQ ID NO:1.

32. (New) The method according to claim 6, wherein the nucleic acid comprises at least 20 nucleic acids of SEQ ID NO:1.

33. (New) The method according to claim 6, wherein the nucleic acid comprises at least 30 nucleic acids of SEQ ID NO:1.

34. (New) The method according to claim 6, wherein the nucleic acid comprises at least 60 nucleic acids of SEQ ID NO:1.

Rule 1.53(b) continuation appln. of  
Serial No. 09/534,072

Atty. Docket No. 4995.0053-01

35. (New) The method according to claim 10, wherein the biological sample is prostate tissue.